OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2002, 09:24:23 ; Search time 265 Seconds
(without alignments)
2838.368 Million cell updates/sec

Title: US-09-765-034-2
Perfect score: 1747
Sequence: 1 MLGIMAWNATCKNWLAAEAA.....KSLTSFSRWAHELLLSFREK 334

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09765034_@CGN_1_1_0_@runat_05122002_132011_21333 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	
1	1737	99.4	1005	21	AAD01135	Hum.
2	1737	99.4	1005	21	AAA46036	Human
3	1737	99.4	1436	24	ABL90790	Human
4	1737	99.4	1542	24	AAD24958	Human G-
5	1725	98.7	1996	18	AAT71900	Human puri... r
6	1709	97.8	1385	21	AAC81122	Human secret... pro
7	1709	97.8	1428	18	AAT75146	Human ATP receptor
8	1231.5	70.5	1543	24	ABK12957	DNA sequence of mo
9	498	28.5	6721	24	AAS18599	Purinergic recepto
10	493	28.2	6721	24	AAS18600	Purinergic recepto
11	477	27.3	1011	24	AAL43942	Human G protein-co
12	477	27.3	1014	22	AAS07948	Human cDNA encodin
13	477	27.3	1014	24	ABQ78847	Human G-protein co
14	477	27.3	1014	24	ABN85630	Human P2Y-like rec
15	477	27.3	1014	24	AAD34278	Human AXOR89 (G-pr
16	477	27.3	1014	24	ABK11381	Human DNA encoding
17	477	27.3	1014	24	AAK98323	Human purinergic-r
18	477	27.3	1014	24	AAD26370	Human G-protein co
19	477	27.3	1288	24	ABL56197	Human P2Y1-li enco
20	477	27.3	5435	24	ABL56198	Human P2Y1-li enco
21	477	27.3	9905	24	AAK98324	Human purinergic-r
22	470	26.9	1729	22	AAS08362	Human cDNA encodin
23	470	26.9	1729	23	ABV24026	Human prostate exp
24	470	26.9	1729	23	ABV25767	Human prostate exp
25	470	26.9	1729	23	ABV29909	Human prostate exp
26	470	26.9	1729	23	ABV30024	Human prostate exp
27	433	24.8	1020	22	AAH51011	Human nGPCR54 codi
28	395.5	22.6	831	24	ABN85629	Human P2Y-like rec
29	386	22.1	2138	24	AAD32937	Mus musculus GPCR
30	386	22.1	2138	24	AAD32944	Mus musculus GPCR
31	385	22.0	2025	22	AAD04980	Human purinergic r
32	384	22.0	993	24	AAH77276	Human G-protein co
c 33	384	22.0	1026	24	AAS98140	Human DNA for pote
34	384	22.0	1039	22	AAS10778	DNA encoding cyste
35	384	22.0	1041	22	AAH26608	Human P2Y-like GPC
36	384	22.0	1041	22	AAS07941	Human cDNA encodin
37	384	22.0	1041	24	AAD28591	Human CysLT2 GPCR
38	384	22.0	1041	24	AAH77279	Human G-protein co
39	384	22.0	1260	22	AAD13709	Human G-protein co
40	384	22.0	1430	22	AAH26609	Human P2Y-like GPC
41	384	22.0	1430	24	AAS16243	Human CysLT2-like
42	384	22.0	1438	24	ABA92899	Human LTD4-like G
43	384	22.0	1625	22	AAD19577	Human G-protein co
44	384	22.0	1700	24	ABK94908	Human novel polynu
45	384	22.0	2720	24	AAS98072	Human DNA for pote

ALIGNMENTS

RESULT 1
AAD01135
ID AAD01135 standard; cDNA; 1005 BP.
XX
AC AAD01135;
XX
DT 02-NOV-2000 (first entry)
XX
DE Human orphan G protein-coupled receptor hCHN10 cDNA.
XX
KW Human; orphan G protein-coupled receptor; GPCR; hCHN10; drug screening;
KW transmembrane receptor; expressed sequence tag; EST; signal cascade; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
FT 1..1005
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FT                   /product= "hCHN10"
FT                   /note= "Human orphan G protein-coupled receptor"
XX
PN   WO200031258-A2.
XX
PD   02-JUN-2000.
XX
PF   13-OCT-1999;    99WO-US23687.
XX
PR   20-NOV-1998;    98US-0109213.
PR   16-FEB-1999;    99US-0120416.
PR   26-FEB-1999;    99US-0121852.
PR   12-MAR-1999;    99US-0123946.
PR   12-MAR-1999;    99US-0123949.
PR   28-MAY-1999;    99US-0136436.
PR   28-MAY-1999;    99US-0136437.
PR   28-MAY-1999;    99US-0136439.
PR   28-MAY-1999;    99US-0136567.
PR   28-MAY-1999;    99US-0137127.
PR   28-MAY-1999;    99US-0137131.
PR   28-MAY-1999;    99US-0141448.
PR   29-JUN-1999;    99US-0156555.
PR   29-SEP-1999;    99US-0156633.
PR   29-SEP-1999;    99US-0156634.
PR   29-SEP-1999;    99US-0156653.
PR   29-SEP-1999;    99US-0157280.
PR   01-OCT-1999;    99US-0157281.
PR   01-OCT-1999;    99US-0157282.
PR   01-OCT-1999;    99US-0157293.
PR   01-OCT-1999;    99US-0157294.
PR   01-OCT-1999;    99US-0416760.
PR   12-OCT-1999;    99US-0417044.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Chen R, Dang HT, Liaw CW, Lin I;
XX
DR   WPI; 2000-400068/34.
DR   P-PSDB; AAY71308.
XX
PT   Novel human orphan G protein-coupled receptors and the encoding cDNAs
PT   for use in the identification of G protein-coupled receptor agonists -
XX
PS   Claim 69; Page 86; 102pp; English.
XX
CC   The present sequence is a cDNA encoding hCHN10, an endogenous human
CC   orphan G protein-coupled receptor (GPCR), expressed in kidney and
CC   thyroid. The hCHN10 cDNA was identified using the human EST (expressed
CC   sequence tag) 1365839 as a probe. The orphan GPCR of the invention, like
CC   all GPCRs has seven transmembrane alpha helices with an extracellular
CC   N-terminus and an intracellular C-terminus. However, no endogenous
CC   ligands has yet been identified for the proteins of the invention. The
CC   orphan GPCRs may be used in the identification of their endogenous
CC   ligands, and to screen potential GPCR agonists and antagonists for use as
CC   pharmaceutical agents. The proteins may also be used in the study of
CC   GPCR-mediated signalling cascades, and to elucidate their precise role in
CC   normal and diseased human conditions. Nucleic acid encoding human orphan
CC   GPCRs may be used for tissue localisation expression analysis to provide
CC   information about their function in healthy and pathological states.
XX
SQ   Sequence 1005 BP; 248 A; 236 C; 196 G; 325 T; 0 other;
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Alignment Scores:		Length:	1005
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Best Local Similarity:	99.70%	Indels:	0
Query Match:	99.43%	Gaps:	0
DB:	21		

US-09-765-034-2 (1-334) x AAD01135 (1-1005)

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Qy      21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40

Db      61 CTGGAAAAGTACTACCTTTCCATTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGA 120

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Qy      61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80

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Qy     121 TyrLeuIleIleLysTyrProPheArgGluHisLeuGlnLysLysGluPheAlaIle 140

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Qy     161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180

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Qy     201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220

Db     601 TTTGTGATGTGTTTCTTTTATTACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAG 660

Qy     221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240

Db     661 GTTGCTACTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATC 720

Qy     241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260

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Qy     261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280

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Qy     321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334

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```
RESULT 2
AAA46036
ID   AAA46036 standard; cDNA; 1005 BP.
XX
AC   AAA46036;
XX
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DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hCHN10 encoding cDNA SEQ ID NO:37.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant; ss.
XX
OS Homo sapiens.
XX
PN WO200022131-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
DR WPI; 2000-317986/27.
DR P-PSDB; AAB02842.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents -
XX
PS Example 1; Page 116; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 1005 BP; 248 A; 236 C; 196 G; 325 T; 0 other;

Alignment Scores:

Pred. No.:	2.05e-160	Length:	1005
Score:	1737.00	Matches:	333
Percent Similarity:	99.70%	Conservative:	0
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.43%	Indels:	0
DB:	21	Gaps:	0

US-09-765-034-2 (1-334) x AAA46036 (1-1005)

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Qy      21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40
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Qy      41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
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Qy     121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
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Qy     141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
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Qy     161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
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Qy     201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
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Qy     221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240
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Qy     241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
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Qy     301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
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Qy     321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
           ||||||||||||||||||||||||||||||||||||||||||
Db     961 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAAG 1002
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RESULT 3
ABL90790

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ID   ABL90790 standard; cDNA; 1436 BP.
XX
AC   ABL90790;
XX
DT   24-MAY-2002  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 1352.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200190304-A2.
XX
PD   29-NOV-2001.
XX
PF   18-MAY-2001; 2001WO-US16450.
XX
PR   19-MAY-2000; 2000US-205515P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CE,  Rosen CA;
XX
DR   WPI; 2002-122018/16.
DR   P-PSDB; ABB90381.
XX
PT   Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT   prevention of neural, immune system, muscular, reproductive,
PT   gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT   disorders -
XX
PS   Claim 4; SEQ ID NO 1352; 2081pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC   (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC   in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC   and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC   epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC   and parasitic infections.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1436 BP; 397 A; 309 C; 289 G; 441 T; 0 other;

Alignment Scores:
Pred. No.:                3.29e-160     Length:          1436
Score:                    1737.00       Matches:         333
Percent Similarity:       99.70%        Conservative:    0
Best Local Similarity:    99.70%        Mismatches:      1
Query Match:              99.43%        Indels:          0
DB:                       24            Gaps:            0

US-09-765-034-2 (1-334) x ABL90790 (1-1436)

Qy       1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      93 ATGCTGGGGATCATGGCATGGAATGCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCC 152

Qy      21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     153 CTGGAAAAGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGA 212

Qy      41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     213 AATACCATTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATT 272

Qy      61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     273 TATCTCTTTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATA 332

Qy      81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     333 AGGAGTTATGCCAATGGAAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATAT 392

Qy     101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     393 GTGCTTCATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGA 452

Qy     121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     453 TACTTGATAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATT 512

Qy     141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     513 TTAATCTCCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTT 572

Qy     161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     573 ATAAATCCTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGAC 632

Qy     181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     633 CCCAACTACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTT 692

Qy     201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     693 TTTGTGATGTGTTTCTTTTATTACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAG 752

Qy     221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     753 GTTGCTACTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATC 812

Qy     241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
           |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db     813 TTCTCTGTGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTG 872

Qy     261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     873 GGGAGTTGGAAGCAGTATCAGTGCACTCAGGTCGTCATCAACTCCTTTTACATTGTGACA 932

Qy     281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     933 CGGCCTTTGGCCTTTCTGAACAGTGTCATCAACCCTGTCTTCTATTTTCTTTTGGGAGAT 992

Qy     301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     993 CACTTCAGGGACATGCTGATGAATCAACTGAGACACAACTTCAAATCCCTTACATCCTTT 1052

Qy     321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
           ||||||||||||||||||||||||||||||||||||||||||
Db    1053 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAAG 1094

RESULT 4
AAD24958
ID   AAD24958 standard; cDNA; 1542 BP.
XX
AC   AAD24958;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor-3 (GCREC-3) cDNA.
```

XX
KW Human; G-protein coupled receptor-3; GCREC-3; therapy; cancer; stroke;
KW cell proliferative disorder; neurological; epilepsy; Parkinson's disease;
KW Alzheimer's disease; inflammation; thyroiditis; haemolytic anaemia; AIDS;
KW Acquired Immune Deficiency Syndrome; dementia; nootropic; cholelithiasis;
KW multiple sclerosis; atherosclerosis; angina pectoris; gastroenteritis;
KW diabetes; ulcer; viral infection; immunosuppressive; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 63..1202
FT /*tag= a
FT /product= "Human GCREC-3 protein"
XX
PN WO200198351-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US19275.
XX
PR 16-JUN-2000; 2000US-212483P.
PR 22-JUN-2000; 2000US-213954P.
PR 29-JUN-2000; 2000US-215209P.
PR 07-JUL-2000; 2000US-216595P.
PR 14-JUL-2000; 2000US-218936P.
PR 19-JUL-2000; 2000US-219154P.
PR 21-JUL-2000; 2000US-220141P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Baughn MR, Hafalia AJA, Nguyen DB, Gandhi AR, Kallick DA;
PI Griffin JA, Yue H, Khan FA, Patterson C, Lu DAM, Tribouley CM;
PI Lu Y, Walia NK, Graul R, Yao MG, Yang J, Ramkumar J, Au-Young J;
PI Elliott VS, Hernandez R, Walsh RT, Borowsky ML, Thornton M, He A;
XX
DR WPI; 2002-075627/10.
DR P-PSDB; AAE15633.
XX
PT Isolated human G-protein coupled receptor polypeptides and the use of
PT these sequences in the diagnosis, treatment and prevention of diseases
PT and in the assessment of exogenous compounds on the expression of the
PT receptors -
XX
PS Claim 11; Page 133; 143pp; English.
XX
CC The invention relates to isolated human G-protein coupled receptor
CC (GCREC) polypeptides and their biologically active fragments. GCREC and
CC protein is useful in treating a disease or condition associated with an
CC increase or decrease in expression of functional GCREC. The GCREC's are
CC useful in the diagnosis, treatment and prevention of cell proliferative
CC disorders (cancer, leukaemia, melanoma); neurological disorders (stroke,
CC epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune
CC inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple
CC sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris),
CC gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis),
CC metabolic disorders (diabetes); viral infections (herpes virus) and in
CC the assessment of the effects of exogenous compounds on the expression
CC of the nucleic acid and amino acid sequences. The present sequence is
CC human GCREC-3 cDNA.
XX
SQ Sequence 1542 BP; 428 A; 327 C; 315 G; 472 T; 0 other;

Alignment Scores:

Pred. No.:	3.61e-160	Length:	1542
Score:	1737.00	Matches:	333
Percent Similarity:	99.70%	Conservative:	0
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.43%	Indels:	0
DB:	24	Gaps:	0

US-09-765-034-2 (1-334) x AAD24958 (1-1542)

```
Qy       1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAla 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198 ATGCTGGGGATCATGGCATGGAATGCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCC 257

Qy      21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     258 CTGGAAAAGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGA 317

Qy      41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     318 AATACCATTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATT 377

Qy      61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     378 TATCTCTTTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATA 437

Qy      81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     438 AGGAGTTATGCCAATGGAAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATAT 497

Qy     101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     498 GTGCTTCATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGA 557

Qy     121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     558 TACTTGATAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATT 617

Qy     141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     618 TTAATCTCCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTT 677

Qy     161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     678 ATAAATCCTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGAC 737

Qy     181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     738 CCCAACTACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTT 797

Qy     201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     798 TTTGTGATGTGTTTCTTTTATTACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAG 857

Qy     221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     858 GTTGCTACTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATC 917

Qy     241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     918 TTCTCTGTGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTG 977

Qy     261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     978 GGGAGTTGGAAGCAGTATCAGTGCACTCAGGTCGTCATCAACTCCTTTTACATTGTGACA 1037

Qy     281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1038 CGGCCTTTGGCCTTTCTGAACAGTGTCATCAACCCTGTCTTCTATTTTCTTTTGGGAGAT 1097

Qy     301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1098 CACTTCAGGGACATGCTGATGAATCAACTGAGACACAACTTCAAATCCCTTACATCCTTT 1157

Qy     321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
          ||||||||||||||||||||||||||||||||||||||||||
Db    1158 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAAG 1199
```

RESULT 5
AAT71900
ID AAT71900 standard; cDNA; 1996 BP.
XX
AC AAT71900;

```
XX
DT   11-SEP-1997  (first entry)
XX
DE   Human purinergic receptor P2U2 cDNA.
XX
KW   P2U2 receptor; purinergic receptor; diagnosis; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             625..1629
FT                   /*tag= a
FT
XX
PN   WO9720045-A2.
XX
PD   05-JUN-1997.
XX
PF   08-NOV-1996;    96WO-US18175.
XX
PR   15-NOV-1995;    95US-0559524.
PR   15-NOV-1995;    95US-0006782.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Conley PB,  Jantzen H;
XX
DR   WPI; 1997-310601/28.
DR   P-PSDB; AAW19854.
XX
PT   New isolated purinergic receptor sub-type  - used to develop
PT   products for diagnosis and therapy, e.g. for screening for agonists
PT   and antagonists which can modulate activation
XX
PS   Claim 3; Fig 1A-C; 36pp; English.
XX
CC   A cDNA clone (AAT71900) codes for a novel human purinergic receptor
CC   subtype, designated P2U2 receptor (AAW19854), that is abundantly
CC   expressed in kidney and in many cell lines of megakaryocytic or
CC   erythroleukaemic origin and which is activated by ATP, UDP, UTP and
CC   UDP.  The clone was obtd. by amplifying DAMI (ATCC CRL 9792) cell
CC   cDNA using primers (see also AAT72104-05) based on transmembrane
CC   regions of mouse P2u and chicken P2Y1 receptors, and use of the PCR
CC   product to  screen the DAMI cDNA library to isolate the full-length
CC   clone.  P2U2 nucleic acids can be used in the recombinant prodn. of
CC   P2U2 receptor polypeptides and as probes.
XX
SQ   Sequence 1996 BP; 513 A; 454 C; 381 G; 647 T; 1 other;

Alignment Scores:
Pred. No.:                  7.57e-159      Length:          1996
Score:                      1725.00        Matches:         331
Percent Similarity:         99.10%         Conservative:    0
Best Local Similarity:      99.10%         Mismatches:      3
Query Match:                98.74%         Indels:          0
DB:                         18             Gaps:            0

US-09-765-034-2 (1-334) x AAT71900 (1-1996)

Qy       1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     625 ATGCTGGGGATCATGGCATGGAATGCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCC 684

Qy      21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     685 CTGGAAAAGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGA 744

Qy      41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     745 AATACCATTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATT 804

Qy      61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     805 TATCTCTTTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATA 864

Qy      81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     865 AGGAGTTATGCCAATGGAAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATAT 924

Qy     101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     925 GTGCTTCATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGA 984

Qy     121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     985 TACTTGATAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATT 1044

Qy     141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1045 TTAATCTCCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTT 1104

Qy     161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1105 ATAAATCCTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGAC 1164

Qy     181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1165 CCCAACTACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTT 1224

Qy     201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1225 TTTGTGATGTGTTTCTTTTATTACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAG 1284

Qy     221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1285 GTTGCTACTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATC 1344

Qy     241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
           |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1345 TTCTCTGTGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTG 1404

Qy     261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1405 GGGAGTTGGAAGCAGTATCAGTGCACTCAGGTCGTCATCAACTCCTTTTACATTGTGACA 1464

Qy     281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
           |||  |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1465 CGGGCTTTGGGCTTTCTGAACAGTGTCATCAACCCTGTCTTCTATTTTCTTTTGGGAGAT 1524

Qy     301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1525 CACTTCAGGGACATGCTGATGAATCAACTGAGACACAACTTCAAATCCCTTACATCCTTT 1584

Qy     321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
           ||||||||||||||||||||||||||||||||||||||||||
Db    1585 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAAG 1626

RESULT 6
AAC81122
ID   AAC81122 standard; cDNA; 1385 BP.
XX
AC   AAC81122;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Human secreted protein gene 37 SEQ ID NO:47.
XX
KW   Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW   antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW   cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW   fungicide; ophthalmological; vulnerary; gene therapy; autoimmune disease;
KW   hyperproliferative disorder; cardiovascular disorder; angiogenesis;
KW   cerebrovascular disorder; nervous system disorder; infection; skin aging;
KW   ocular disorder; wound healing; food additive; preservative; ss.
XX
OS   Homo sapiens.
XX
```

PN WO200061628-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US09070.
XX
PR 09-APR-1999; 99US-0128695.
PR 14-JAN-2000; 2000US-0176052.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-619228/59.
DR P-PSDB; AAB45344.
XX
PT New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Claim 1; Page 412; 454pp; English.
XX
CC The polynucleotide sequences given in AAC81086 to AAC81134 encode the
CC human secreted proteins given in AAB45308 to AAB45356. AAB45357 to
CC AAB45384 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
CC cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
CC neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
CC and vulnerary. The polynucleotides and polypeptides can be used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases, hyperproliferative disorders, cardiovascular
CC disorders, cerebrovascular disorders, angiogenesis, nervous system
CC disorders, infections caused by bacteria, viruses and fungi and ocular
CC disorders. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. AAC81077 to AAC81085 and AAB45307 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 1385 BP; 385 A; 296 C; 275 G; 429 T; 0 other;

Alignment Scores:

Pred. No.:	1.71e-157	Length:	1385
Score:	1709.00	Matches:	332
Percent Similarity:	99.40%	Conservative:	0
Best Local Similarity:	99.40%	Mismatches:	2
Query Match:	97.82%	Indels:	1
DB:	21	Gaps:	0

US-09-765-034-2 (1-334) x AAC81122 (1-1385)

```
Qy       1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49 ATGCTGGGGATCATGGCATGGAATGCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCC 108

Qy      21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 CTGGAAAAGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGA 168

Qy      41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 AATACCATTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATT 228

Qy      61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 TATCTCTTTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATA 288

Qy      81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 AGGAGTTATGCCAATGGAAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATAT 348

Qy     101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 GTGCTTCATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGA 408

Qy     121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 TACTTGATAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATT 468

Qy     141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     469 TTAATCTCCTTGGCCATTTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTT 528

Qy     161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     529 ATAAATCCTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGAC 588

Qy     181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     589 CCCAACTACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTT 648

Qy     201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     649 TTTGTGATGTGTTTCTTTTATTACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAG 708

Qy     221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     709 GTTGCTACTGCTCTGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATC 768

Qy     241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     769 TTCTCTGTGCTTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTG 828

Qy     261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     829 GGGAGTTGGAAGCAGTATCAGTGCACTCAGGTCGTCATCAACTCCTTTTACATTGTGACA 888

Qy     281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     889 CG-CCTTTGGCCTTTCTGAACAGTGTCATCAACCCTGTCTTCTATTTTCTTTTGGGAGAT 947

Qy     301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     948 CACTTCAGGGACATGCTGATGAATCAACTGAGACACAACTTCAAATCCCTTACATCCTTT 1007

Qy     321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
           ||||||||||||||||||||||||||||||||||||||||||
Db    1008 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAAG 1049
```

RESULT 7
AAT75146
ID AAT75146 standard; cDNA; 1428 BP.
XX
AC AAT75146;
XX
DT 07-OCT-1997 (first entry)
XX
DE Human ATP receptor cDNA.
XX
KW ATP receptor; G-protein coupled receptor; agonist; antagonist; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 92..1096
FT /*tag= a

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FT                   /transl_except= (pos:725..727, aa:Ser)
FT                   /transl_except= (pos:764..766, aa:Ser)
FT                   /transl_except= (pos:820..822, Xaa)
FT                   /note= "Xaa = unknown"
FT   primer_bind     complement (92..100)
FT                   /*tag=  b
FT                   /note= "binding site for primer used to amplify
FT                          cDNA for baculovirus expression"
FT   primer_bind     complement (92..109)
FT                   /*tag=  c
FT                   /note= "binding site for primers used to amplify
FT                          cDNA for bacterial or COS expression"
FT   primer_bind     1076..1095
FT                   /*tag=  d
FT                   /note= "binding site for primer used to amplify
FT                          cDNA for COS expression"
FT   primer_bind     1079..1096
FT                   /*tag=  e
FT                   /note= "binding site for primer used to amplify
FT                          cDNA for bacterial expression"
FT   primer_bind     1085..1096
FT                   /*tag=  f
FT                   /note= "binding site for primer used to amplify
FT                          cDNA for baculovirus expression"
XX
PN   WO9724929-A1.
XX
PD   17-JUL-1997.
XX
PF   11-JAN-1996;   96WO-US00392.
XX
PR   11-JAN-1996;   96WO-US00392.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Li Y;
XX
DR   WPI; 1997-372505/34.
DR   P-PSDB; AAW22732.
XX
PT   Isolated human ATP receptor - agonists and antagonists of which are
PT   useful in treatment of, e.g. asthma, hypertension, arterial
PT   thrombosis and psychotic and neurological disorders
XX
PS   Claim 7; Fig 1A-C; 53pp; English.
XX
CC   A cDNA clone (AAT75146) codes for human ATP receptor (AAW22732), a
CC   polypeptide structurally related to the G protein-coupled receptor
CC   family.  It was discovered in a human placenta cDNA library.
CC   cDNA encoding the mature receptor, deposited as ATCC 97333, can
CC   be expressed in bacterial (e.g. E. coli), mammalian (e.g. COS) or
CC   insect (e.g. Sf9) host cells and used to screen for agonists and
CC   antagonists useful in the treatment of a variety of disorders.
CC   It can also be used to identify a mutation in an ATP receptor gene
CC   and thus to diagnose diseases, or susceptibility to diseases,
CC   related to ATP receptor underexpression.
XX
SQ   Sequence 1428 BP; 394 A; 308 C; 290 G; 435 T; 1 other;

Alignment Scores:
Pred. No.:                1.78e-157      Length:          1428
Score:                    1709.00        Matches:         327
Percent Similarity:       98.80%         Conservative:    3
Best Local Similarity:    97.90%         Mismatches:      4
Query Match:              97.82%         Indels:          0
DB:                       18             Gaps:            0

US-09-765-034-2 (1-334) x AAT75146 (1-1428)

Qy       1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      92 ATGCTGGGGATCATGGCATGGAATGCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCC 151

Qy      21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152 CTGGAAAAGTACTACCTTTCCATTTTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGA 211

Qy      41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     212 AATACCATTGTTGTTTACGGCTACATCTTCTCTCTGAAGAACTGGAACAGCAGTAATATT 271

Qy      61 TyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     272 TATCTCTTTAACCTCTCTGTCTCTGACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATA 331

Qy      81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     332 AGGAGTTATGCCAATGGAAACTGGATATATGGAGACGTGCTCTGCATAAGCAACCGATAT 391

Qy     101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     392 GTGCTTCATGCCAACCTCTATACCAGCATTCTCTTTCTCACTTTTATCAGCATAGATCGA 451

Qy     121 TyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIle 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     452 TACTTGATAATTAAGTATCCTTTCCGAGAACACCTTCTGCAAAAGAAAGAGTGTGCTATT 511

Qy     141 LeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeu 160
           ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db     512 TTAATCTCCTTGGCCATGTGGGTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCTT 571

Qy     161 IleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     572 ATAAATCCTGTTATAACTGACAATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGAC 631

Qy     181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     632 CCCAACTACAACCTCATTTACAGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTT 691

Qy     201 PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
           ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db     692 TTTGTGATGTGTTTCTTTTATTACAAGATTGCCTCCTTCCTAAAGCAGAGGAATAGGCAG 751

Qy     221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIle 240
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db     752 GTTGCTACTGCCTCGCCCCTTGAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATC 811

Qy     241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
           |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     812 TTCTCTGTGCYTTTTACACCCTATCACGTCATGCGGAATGTGAGGATCGCTTCACGCCTG 871

Qy     261 GlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     872 GGGAGTTGGAAGCAGTATCAGTGCACTCAGGTCGTCATCAACTCCTTTTACATTGTGACA 931

Qy     281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
           |||||||:::||||||||||||||||||||||||||||||||||||||:::|||||||||
Db     932 CGGCCTGTGGCCTTTCTGAACAGTGTCATCAACCCTGTCTTCTATTTTCTTGTGGGAGAT 991

Qy     301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     992 CACTTCAGGGACATGCTGATGAATCAACTGAGACACAACTTCAAATCCCTTACATCCTTT 1051

Qy     321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
           ||||||||||||||||||||||||||||||||||||||||||
Db    1052 AGCAGATGGGCTCATGAACTCCTACTTTCATTCAGAGAAAAG 1093

RESULT 8
ABK12957
ID   ABK12957 standard; DNA; 1543 BP.
XX
AC   ABK12957;
XX
DT   09-APR-2002  (first entry)
XX
DE   DNA sequence of mouse G-protein coupled receptor TGR18 gene.
```

```
XX
KW   Mouse; G-protein coupled; receptor; GPCR; TGR18; kidney disease;
KW   signal transduction modulator; cerebral cavernous malformation;
KW   hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;
KW   nephritis; hypertension; liver disease; cirrhosis; blood disorder;
KW   spleen-associated disorder; immune disorder; gene; ds.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             44..997
FT                   /*tag=  a
FT                   /product= "Mouse G-protein coupled receptor TGR18"
XX
PN   WO200200719-A2.
XX
PD   03-JAN-2002.
XX
PF   25-JUN-2001; 2001WO-US20363.
XX
PR   23-JUN-2000; 2000US-213461P.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Lin DC,  Zhao J,  Chen J,  Cutler G;
XX
DR   WPI; 2002-147880/19.
DR   P-PSDB; AAU74904.
XX
PT   New G-protein coupled receptor polypeptides, useful for identifying
PT   modulators of signal transduction for treating kidney disease,
PT   hyperlipidemia, obesity, dyslexia and cardiac myxoma
XX
PS   Claim 18; Page 58; 78pp; English.
XX
CC   The present invention relates to a new G-protein coupled receptor (GPCR)
CC   polypeptide comprising greater than 70% amino acid sequence identity to
CC   the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2,
CC   human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18
CC   or 90% amino acid sequence identity to human novel edg receptor protein,
CC   as defined in the specification. The GPCR covalently linked to a solid
CC   phase is useful for identifying a compound that modulates signal
CC   transduction. The identified compounds are useful for treating
CC   kidney disease, cerebral cavernous malformations, hyperlipidemia,
CC   obesity, dyslexia and cardiac myxoma. The molecules of the invention are
CC   useful for diagnosing disorders or conditions such as kidney-related
CC   conditions or diseases such as renal failure, nephritis, nephrotic
CC   syndrome, asymptomatic urinary abnormalities, renal tubule defects,
CC   hypertension and nephrolithiasis, liver-related disease or condition
CC   e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice
CC   and spleen-associated disorders or conditions e.g. splenic enlargement,
CC   immune disorders, blood disorders and others. Modulation of the
CC   polypeptide of the invention is useful to treat or prevent any of the
CC   above conditions or diseases. The present nucleic acid sequence encodes
CC   the mouse GPCR TGR18 protein of the invention. This sequence encodes one
CC   of seven novel G protein coupled receptors of the invention (ABK12957-
CC   ABK12964).
XX
SQ   Sequence 1543 BP; 438 A; 352 C; 293 G; 460 T; 0 other;

Alignment Scores:
Pred. No.:              9.67e-111      Length:          1543
Score:                  1231.50        Matches:         227
Percent Similarity:     85.13%         Conservative:    42
Best Local Similarity:  71.84%         Mismatches:      46
Query Match:            70.49%         Indels:          1
DB:                     24             Gaps:            1

US-09-765-034-2 (1-334) x ABK12957 (1-1543)

Qy       5 MetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr 24
           ||||||   |||   :::|||:::||||||||||||||   ||||||   |||   ||||||
Db      44 ATGGCACAGAATTTATCTTGTGAGAATTGGTTGGCAACAGAGGCTATCTTGAATAAGTAC 103

Qy      25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44
           |||||||||   ||||||   |||||||||:::   |||:::|||||||||      |||
Db     104 TACCTCTCTGCATTTTATGCAATCGAGTTCATTTTTGGACTGCTTGGGAATGTCACTGTG 163

Qy      45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64
           |||:::|||||:::|||   :::||||||||||||||||||:::||||||||||||||||
Db     164 GTGTTCGGCTACCTCTTCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTTAAC 223

Qy      65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
           ||||||:::||||||   |||||||||||||||||||||:::||||||:::|||||||||
Db     224 CTTTCCATCTCTGACTTTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCC 283

Qy      85 AsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAla 104
           |||            ||||||||||||||||||||||||||||||||||||||||||||
Db     284 AATGATAAGGGGACCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACC 343

Qy     105 AsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIle 124
           ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||:::::
Db     344 AACCTCTACACCAGCATCCTCTTCCTCACTTTCATTAGCATGGACCGATATCTGCTCATG 403

Qy     125 LysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIleLeuIleSerLeu 144
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db     404 AAGTACCCTTTCCGAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTG 463

Qy     145 AlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProVal 164
           |||:::|||   |||||||||||||||:::|||||||:::|||      ||||||   |||
Db     464 GCTGTCTGGGCCTTAGTGACCTTAGAAGTTCTACCCATGCTCACTTTCATCAATTCTGTC 523

Qy     165 IleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsn 184
                 :::   |||:::   |||   |||:::||||||||||||:::|||   :::|||
Db     524 CCAAAAGAAGAGGGCAGTAACTGCATCGACTATGCAAGTTCTGGAAACCCTGAACACAAT 583

Qy     185 LeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCys 204
           ||||||||||||:::|||||||||||||||||||||||||||||||||   |||||||||
Db     584 CTCATTTACAGCCTCTGCCTGACTTTGTTGGGCTTCCTAATTCCTCTCTCTGTGATGTGC 643

Qy     205 PhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAla 224
           |||||||||||||||:::   :::|||||||||:::|||:::::::|||   |||||||||
Db     644 TTCTTCTACTACAAGATGGTAGTCTTCTTAAAGAGGAGGAGCCAGCAGCAAGCAACTGCC 703

Qy     225 LeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerValPro 244
           ||||||||||:::|||||||      ||||||:::::|||||||||||||||||||:::
Db     704 CTGCCACTGGACAAACCCCAACGCCTGGTGGTCCTGGCGGTTGTGATCTTCTCTATACTC 763

Qy     245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
           |||||||||||||||:::|||||||||:::|||||||||||||||||||   ||||||
Db     764 TTCACACCCTATCATATCATGCGCAATTTGAGGATCGCCTCACGCCTGGATAGTTGGCCA 823

Qy     265 GlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThrArgProLeuAla 284
           |||   |||||||||      |||   |||   |||   :::|||||||||||||||||
Db     824 CAA---GGATGTACACAGAAGGCCATCAAATCTATATACACACTGACACGGCCTCTGGCC 880

Qy     285 PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp 304
           ||||||||||||   ||||||||||:::|||||||||||||:::|||||||||||:::
Db     881 TTTCTGAACAGTGCCATCAATCCCATCTTCTACTTCCTCATGGGAGACCATTACAGAGAG 940

Qy     305 MetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
           ||||||:::::::::   |||      ||||||||||||||||||||
Db     941 ATGCTGATTAGTAAGTTCAGACAATACTTCAAGTCCCTTACATCCTTC 988

RESULT 9
AAS18599
ID   AAS18599 standard; DNA; 6721 BP.
XX
AC   AAS18599;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Purinergic receptor P2Y, G-protein coupled 1 gene.
XX
KW   Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;
KW   coagulant; platelet aggregation; haplotyping; drug screening;
```

```
KW   transgenic animal; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (3640,T)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism"
FT   CDS             4002..5123
FT                   /*tag= c
FT                   /product= "P2RY1"
FT                   /note= "Purinergic receptor P2Y, G-protein coupled 1"
FT   variation       replace (3883,T)
FT                   /*tag= d
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (3885,A)
FT                   /*tag= e
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (3893,A)
FT                   /*tag= f
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4049,T)
FT                   /*tag= g
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4058,T)
FT                   /*tag= h
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4102,T)
FT                   /*tag= i
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4136,G)
FT                   /*tag= j
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4199,T)
FT                   /*tag= k
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4689,C)
FT                   /*tag= l
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4786,G)
FT                   /*tag= m
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (4787,G)
FT                   /*tag= n
FT                   /standard_name= "Single nucleotide polymorphism"
FT   variation       replace (5158,G)
FT                   /*tag= o
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200190117-A2.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-US16432.
XX
PR   19-MAY-2000; 2000US-205996P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kazemi A, Koshy B, Tanguay DA;
XX
DR   WPI; 2002-083074/11.
DR   P-PSDB; AAU10983.
XX
PT   New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene
PT   polymorphic variants, useful e.g. in studying the expression and
PT   function of P2RY1 and screening candidate drugs for treating diseases
PT   related to P2RY1 activity -
XX
PS   Disclosure; Fig 1; 79pp; English.
XX
CC   The invention relates to a novel isolated polypeptide comprising a
CC   sequence which is a polymorphic variant of a reference sequence for the
CC   purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its
CC   fragment. The polymorphic variant comprises one or more variant amino
CC   acids selected from valine at a position 34 and glycine at a position
CC   262. The polymorphic variants are useful in studying the expression
CC   and function of P2RY1, in expressing P2RY1 protein for use in screening
CC   for candidate drugs to treat diseases related to P2RY1 activity, in
CC   studying the effect of the variation on the biological activity of
CC   P2RY1, and the binding affinity of candidate drugs targeting P2RY1 for
CC   the treatment of disorders related to platelet aggregation. The
CC   haplotyping methods are useful in validating P2RY1 as a candidate
CC   target for treating a specific condition or disease predicted to be
CC   associated with P2RY1 activity, or in the design of clinical trials of
CC   candidate drugs for treating a specific condition or disease associated
CC   with P2RY1 activity. The transgenic animals are useful for studying
CC   expression of the P2RY1 isogenes in vivo, for in vivo screening and
CC   testing of drugs targeted against P2RY1 protein, and for testing the
CC   efficacy of therapeutic agents and compounds for disorders related to
CC   platelet aggregation in a biological system. The present sequence
CC   represents the coding sequence of human purinergic receptor P2Y,
CC   G-coupled protein 1 (P2RY1).
XX
SQ   Sequence 6721 BP; 1906 A; 1547 C; 1561 G; 1684 T; 23 other;

Alignment Scores:
Pred. No.:                3.55e-38      Length:          6721
Score:                    498.00        Matches:         117
Percent Similarity:       54.49%        Conservative:    59
Best Local Similarity:    36.22%        Mismatches:      130
Query Match:              28.51%        Indels:          17
DB:                       24            Gaps:            7

US-09-765-034-2 (1-334) x AAS18599 (1-6721)

Qy       1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGlu-AlaAl 20
Db    4070 GTCCTGGGGGAACAGCACGGTCGCCTCCACTGCCGCCGTCTCCTCGTCGTTCAAATGCGC 4129

Qy      20 aLeuGluLys--------------TyrTyrLeuSerIlePheTyrGlyIleGluPheVa 35
Db    4130 CTTGACCAAGACGGGCTTCCAGTTTTACTACCTGCCGGCTGTCTACATCTTGGTATTCAT 4189

Qy      35 lValGlyValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTr 55
Db    4190 CATCGGCTTCCTGGGCAACAGCGTGGCCATCTGGATGTTCGTCTTCCACATGAAGCCCTG 4249

Qy      55 pAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysTh 75
Db    4250 GAGCGGCATCTCCGTGTACATGTTCAATTTGGCTCTGGCCGACTTCTTGTACGTGCTGAC 4309

Qy      75 rLeuProMetLeuIleArgSerTyrAlaAsn---GlyAsnTrpIleTyrGlyAspValLe 94
Db    4310 TCTGCCAGCCCTGATCTTCTACTACTTCAATAAAACAGACTGGATCTTCGGGGATGCCAT 4369

Qy      94 uCysIleSerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuTh 114
Db    4370 GTGTAAACTGCAGAGGTTCATCTTTCATGTGAACCTCTATGGCAGCATCTTGTTTCTGAC 4429

Qy     114 rPheIleSerIleAspArgTyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGl 134
Db    4430 ATGCATCAGTGCCCACCGGTACAGCGGTGTGGTGTACCCCCTCAAGTCCCTGGGCCGGCT 4489

Qy     134 nLysLysGluPheAlaIleLeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLe 154
Db    4490 CAAAAAGAAGAATGCGATCTGTATCAGCGTGCTGGTGTGGCTCATTGTGGTGGTGGCGAT 4549

Qy     154 uLeuProIleLeuProLeuIleAsnProValIleThrAspAsnGlyThr---ThrCysAs 173
Db    4550 CTCCCCCATCCTCTTCTACTCAGGTACCGGGGTCCGCAAAAACAAAACCATCACCTGTTA 4609

Qy     173 nAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLe 193
```

```
          |||      |||                          ||||||||||||||||   |||::
Db   4610 CGACACCACCTCAGACGAGTACCTGCGAAGTTATTTCATCTACAGCATGTGCACGACCGT 4669

Qy    193 uLeuGlyPheLeuIleProLeuPheValMet------CysPhePheTyrTyrLysIleAl 211
          :     |||   :::||||||   ::::::      |||:::                 ||
Db   4670 GGCCATGTTCTGTGTCCCCTTGGTGCTGATTCTGGGCTGTTACGGATTAATTGTGAGAGC 4729

Qy    211 aLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuProLeu---GluLysPr 230
          ||||      |||      :::                        ||||||      |||
Db   4730 TTTGATTTACAAAGATCTGGACAACTCT--------------CCTCTGAGGAGAAAATC 4774

Qy    230 oLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThrProTyrHisVa 250
          :::   |||||||||:::   :::   :::|||:::|||   :::   |||:::||||
Db   4775 GATTTACCTGGTAATCATTGTACTGACTGTTTTTGCTGTGTCTTACATCCCTTTCCATGT 4834

Qy    250 lMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThr-- 269
          ||||:::   :::   :::   :::|||||                          |||
Db   4835 GATGAAAACGATGAACTTGAGGGCCCGGCTTGATTTTCAGACCCCAGCAATGTGTGCTTT 4894

Qy    270 -GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerVa 289
               :::   :::   |||   |||||||||   ||||||   |||||||||
Db   4895 CAATGACAGGGTTTATGCCACGTATCAGGTGACAAGAGGTCTAGCAAGTCTCAACAGTTG 4954

Qy    289 lIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMetLeuMetAsnGl 309
          ::::::|||:::   |||||||||   ||||||   ||||||      |||
Db   4955 TGTGGACCCCATTCTCTATTTCTTGGCGGGAGATACTTTCAGAAGGAGACTCTCCCGAGC 5014

Qy    309 nLeuArg 311
             |||
Db   5015 CACAAGG 5021

RESULT 10
AAS18600
ID   AAS18600 standard; DNA; 6721 BP.
XX
AC   AAS18600;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Purinergic receptor P2Y, G-protein coupled 1 gene, generic sequence.
XX
KW   Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;
KW   coagulant; platelet aggregation; haplotyping; drug screening;
KW   transgenic animal; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200190117-A2.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-US16432.
XX
PR   19-MAY-2000; 2000US-205996P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kazemi A,  Koshy B,  Tanguay DA;
XX
DR   WPI; 2002-083074/11.
XX
PT   New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene
PT   polymorphic variants, useful e.g. in studying the expression and
PT   function of P2RY1 and screening candidate drugs for treating diseases
PT   related to P2RY1 activity  -
XX
PS   Claim 20; Page 77-79; 79pp; English.
XX
CC   The invention relates to a novel isolated polypeptide comprising a
CC   sequence which is a polymorphic variant of a reference sequence for the
CC   purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its
CC   fragment. The polymorphic variant comprises one or more variant amino
CC   acids selected from valine at a position 34 and glycine at a position
CC   262. The polymorphic variants are useful in studying the expression
CC   and function of P2RY1, in expressing P2RY1 protein for use in screening
CC   for candidate drugs to treat diseases related to P2RY1 activity, in
CC   studying the effect of the variation on the biological activity of
CC   P2RY1, and the binding affinity of candidate drugs targeting P2RY1 for
CC   the treatment of disorders related to platelet aggregation. The
CC   haplotyping methods are useful in validating P2RY1 as a candidate
CC   target for treating a specific condition or disease predicted to be
CC   associated with P2RY1 activity, or in the design of clinical trials of
CC   candidate drugs for treating a specific condition or disease associated
CC   with P2RY1 activity. The transgenic animals are useful for studying
CC   expression of the P2RY1 isogenes in vivo, for in vivo screening and
CC   testing of drugs targeted against P2RY1 protein, and for testing the
CC   efficacy of therapeutic agents and compounds for disorders related to
CC   platelet aggregation in a biological system. The present sequence
CC   represents the generic coding sequence of human purinergic receptor P2Y,
CC   G-coupled protein 1 (P2RY1), incorporating all possible polymorphisms of
CC   the gene.
XX
SQ   Sequence 6721 BP; 1904 A; 1539 C; 1558 G; 1682 T; 38 other;

Alignment Scores:
Pred. No.:                1.09e-37        Length:          6721
Score:                    493.00          Matches:         116
Percent Similarity:       54.18%          Conservative:    59
Best Local Similarity:    35.91%          Mismatches:      131
Query Match:              28.22%          Indels:          17
DB:                       24              Gaps:            7

US-09-765-034-2 (1-334) x AAS18600 (1-6721)

Qy      1 MetLeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGlu-AlaAl 20
          :::|||||||                    |||:::      |||      :::    ||
Db   4070 GTCCTGGGGGAACAGCACGGTCGCCTCCACTGYCGCCGTCTCCTCGTCGTTCAAATGCGC 4129

Qy     20 aLeuGluLys--------------TyrTyrLeuSerIlePheTyrGlyIleGluPheVa 35
          ||||  |||              |||||||||         |||  :::  |||::
Db   4130 CTTGACSAAGACGGGCTTCCAGTTTTACTACCTGCCGGCTGTCTACATCTTGGTATTCAT 4189

Qy     35 lValGlyValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTr 55
          ::::|||   |||||||||::::::   ::::::  ::::::|||   :::|||   ||
Db   4190 CATCGGCTTYCTGGGCAACAGCGTGGCCATCTGGATGTTCGTCTTCCACATGAAGCCCTG 4249

Qy     55 pAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysTh 75
          |:::      ::::::|||:::|||||||||:::::::::|||      ::::::   ||
Db   4250 GAGCGGCATCTCCGTGTACATGTTCAATTTGGCTCTGGCCGACTTCTTGTACGTGCTGAC 4309

Qy     75 rLeuProMetLeuIleArgSerTyrAlaAsn---GlyAsnTrpIleTyrGlyAspValLe 94
          |||||||  ||||||      |||  |||      :::||||||:::||||||   ::
Db   4310 TCTGCCAGCCCTGATCTTCTACTTCAATAAAACAGACTGGATCTTCGGGGATGCCAT 4369

Qy     94 uCysIleSerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuTh 114
          :|||        |||::::::  |||  |||||||||  ||||||||||||||||||
Db   4370 GTGTAAACTGCAGAGGTTCATCTTTCATGTGAACCTCTATGGCAGCATCTTGTTTCTGAC 4429

Qy    114 rPheIleSerIleAspArgTyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGl 134
          |   ||||||      ||||||      :::   ||||||   :::
Db   4430 ATGCATCAGTGCCCACCGGTACAGCGGTGTGGTGTACCCCCTCAAGTCCCTGGGCCGGCT 4489

Qy    134 nLysLysGluPheAlaIleLeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLe 154
          ||||||:::   ||||||   |||||:::   :::|||:::::|||   :::   ::
Db   4490 CAAAAAGAAGAATGCGATCTGTATCAGCGTGCTGGTGTGGCTCATTGTGGTGGTGGCGAT 4549

Qy    154 uLeuProIleLeuProLeuIleAsnProValIleThrAspAsnGlyThr---ThrCysAs 173
          :   |||||||||                  :::      |||  |||   ||||||
Db   4550 CTCCCCCATCCTCTTCTACTCAGGTACCGGGGTCCGCAAAAACAAAACCATCACCTGTTA 4609

Qy    173 nAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLe 193
          |||       |||                          ||||||||||||||   |||::
Db   4610 CGACACCACCTCAGACGAGTACCTGCGAAGTTATTTCATCTACAGCATGTGCACGACCGT 4669

Qy    193 uLeuGlyPheLeuIleProLeuPheValMet------CysPhePheTyrTyrLysIleAl 211
          :     |||   :::||||||   ::::::      |||:::                 ||
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Db    4670 GGCCATGTTCTGTGTCCCCYTGGTGCTGATTCTGGGCTGTTACGGATTAATTGTGAGAGC 4729

Qy     211 aLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuProLeu---GluLysPr 230
Db    4730 TTTGATTTACAAAGATCTGGACAACTCT--------------CCTCTGAGGAGAAAATC 4774

Qy     230 oLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThrProTyrHisVa 250
Db    4775 GATTTACCTGGKRATCATTGTACTGACTGTTTTTGCTGTGTCTTACATCCCTTTCCATGT 4834

Qy     250 lMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThr-- 269
Db    4835 GATGAAAACGATGAACTTGAGGGCCCGGCTTGATTTTCAGACCCCAGCAATGTGTGCTTT 4894

Qy     270 -GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerVa 289
Db    4895 CAATGACAGGGTTTATGCCACGTATCAGGTGACAAGAGGTCTAGCAAGTCTCAACAGTTG 4954

Qy     289 lIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMetLeuMetAsnGl 309
Db    4955 TGTGGACCCCATTCTCTATTTCTTGGCGGGAGATACTTTCAGAAGGAGACTCTCCCGAGC 5014

Qy     309 nLeuArg 311
Db    5015 CACAAGG 5021
```

```
RESULT 11
AAL43942
ID   AAL43942 standard; DNA; 1011 BP.
XX
AC   AAL43942;
XX
DT   27-SEP-2002  (first entry)
XX
DE   Human G protein-coupled receptor coding sequence.
XX
KW   Human; gene therapy; G protein-coupled receptor; drug development;
KW   central nervous system disease; endocrine disease; metabolic disease;
KW   cancer; respiratory disease; digestive disease; immune disease;
KW   inflammation; infection; circulatory disease; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1011
FT                   /*tag= a
FT                   /partial
FT                   /product= "Human G-protein coupled receptor"
FT                   /note= "No stop codon is given"
XX
PN   WO200257441-A1.
XX
PD   25-JUL-2002.
XX
PF   17-JAN-2002; 2002WO-JP00270.
XX
PR   18-JAN-2001; 2001JP-0010714.
PR   30-MAR-2001; 2001JP-0102484.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Miwa M,  Ito T,  Shintani Y,  Miyajima N;
XX
DR   WPI; 2002-566800/60.
DR   P-PSDB; AAO15399.
XX
PT   Human kidney-originated G protein-coupled receptor protein TGR30 and
PT   encoded DNA, for developing drugs to treat central nervous diseases,
PT   endocrine diseases, metabolic diseases and cancer, including gene
PT   therapy  -
XX
PS   Claim 6; Page 90-91; 98pp; Japanese.
XX
```

```
CC   The invention comprises the amino acid and coding sequence of a human G
CC   protein-coupled receptor. The DNA and protein sequences of the invention
CC   are useful for developing drugs to prevent or treat (gene therapy):
CC   central nervous system diseases; endocrine diseases; metabolic diseases;
CC   cancer; respiratory diseases; digestive diseases; immune diseases;
CC   inflammations; infections; and circulatory diseases. The present DNA
CC   sequence encodes the human G protein-coupled receptor of the invention.
XX
SQ   Sequence 1011 BP; 257 A; 263 C; 188 G; 303 T; 0 other;
```

Alignment Scores:			
Pred. No.:	3.29e-37	Length:	1011
Score:	477.00	Matches:	110
Percent Similarity:	55.88%	Conservative:	61
Best Local Similarity:	35.95%	Mismatches:	123
Query Match:	27.30%	Indels:	12
DB:	24	Gaps:	6

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US-09-765-034-2 (1-334) x AAL43942 (1-1011)

Qy       8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyrTyrLeuSer 27
Db      67 AATTGCACTGATGAAAAC--------------ATCCCACTCAAGATGCACTACCTCCCT 111

Qy      28 IlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyrGly 47
Db     112 GTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACT 171

Qy      48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
Db     172 TACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGC 231

Qy      68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsnGly--- 86
Db     232 ACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAA 291

Qy      87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
Db     292 AACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTG 351

Qy     107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
Db     352 TATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCAC 411

Qy     127 ProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIleLeuIleSerLeuAlaIle 146
Db     412 CCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTG 471

Qy     147 TrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
Db     472 TGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAACAGG 531

Qy     167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle 186
Db     532 ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGG 591

Qy     187 TyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCysPhePhe 206
Db     592 TACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGC 651

Qy     207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db     652 TATACCACGATT---ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG 708

Qy     227 LeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThr 246
Db     709 ---CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTA 765

Qy     247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
Db     766 CCCTTCCATATCTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCA---------ATC 816

Qy     267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
```

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Db    817 AGTTGTTCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCT 876

Qy    286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
Db    877 CTGAACACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCT 936

Qy    306 LeuMetAsnGlnLeuArg 311
Db    937 GTCTGCTCAACAGTGAGA 954

RESULT 12
AAS07948
ID   AAS07948 standard; cDNA; 1014 BP.
XX
AC   AAS07948;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human cDNA encoding G-protein coupled receptor, hRUP21.
XX
KW   Human; G-protein coupled receptor; GPCR; hRUP21; agonist;
KW   inverse agonist; lung cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1014
FT                   /*tag= a
FT                   /product= "hRUP21"
XX
PN   WO200136471-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US31509.
XX
PR   17-NOV-1999;   99US-0166088.
PR   17-NOV-1999;   99US-0166099.
PR   17-NOV-1999;   99US-0166369.
PR   23-DEC-1999;   99US-0171900.
PR   23-DEC-1999;   99US-0171901.
PR   23-DEC-1999;   99US-0171902.
PR   11-FEB-2000; 2000US-0181749.
PR   14-MAR-2000; 2000US-0189258.
PR   14-MAR-2000; 2000US-0189259.
PR   10-APR-2000; 2000US-0195898.
PR   10-APR-2000; 2000US-0195899.
PR   10-APR-2000; 2000US-0196078.
PR   28-APR-2000; 2000US-0200419.
PR   12-MAY-2000; 2000US-0203630.
PR   12-JUN-2000; 2000US-0210741.
PR   12-JUN-2000; 2000US-0210982.
PR   21-AUG-2000; 2000US-0226760.
PR   26-SEP-2000; 2000US-0235418.
PR   26-SEP-2000; 2000US-0235779.
PR   20-OCT-2000; 2000US-0242332.
PR   20-OCT-2000; 2000US-0242343.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Chen R,  Dang HT,  Lowitz KP;
XX
DR   WPI; 2001-355616/37.
DR   P-PSDB; AAU04375.
XX
PT   Endogenous and non-endogenous versions of human G-protein coupled
PT   receptors for direct identification of candidate compounds as agonists,
PT   inverse agonists or partial agonists for use as therapeutic agents -
XX
PS   Claim 55; Page 113-114; 159pp; English.
XX
CC   The sequence encodes a human G-protein coupled receptor (GPCR),
CC   hRUP21 The endogenous and non-endogenous, constitutively activated
CC   versions of human G-protein coupled receptors (GPCR), are useful for
CC   direct identification of candidate compounds as receptor agonists,
CC   inverse agonists or partial agonists having applicability as therapeutic
CC   agents for treating diseases related to GPCR, e.g. lung cancer.
CC   Non-endogenous version of human GPCRs are also utilized in research
CC   settings and in vitro and in vivo system, incorporating GPCRs can be
CC   utilised to elucidate and understand the roles these receptors
CC   play in the human condition, both normal and diseased..
XX
SQ   Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Alignment Scores:
Pred. No.:                3.3e-37      Length:          1014
Score:                    477.00       Matches:         110
Percent Similarity:       55.88%       Conservative:    61
Best Local Similarity:    35.95%       Mismatches:      123
Query Match:              27.30%       Indels:          12
DB:                       22           Gaps:            6

US-09-765-034-2 (1-334) x AAS07948 (1-1014)

Qy      8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyrTyrLeuSer 27
Db     67 AATTGCACTGATGAAAAC--------------ATCCCACTCAAGATGCACTACCTCCCT 111

Qy     28 IlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyrGly 47
Db    112 GTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACT 171

Qy     48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
Db    172 TACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGC 231

Qy     68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsnGly--- 86
Db    232 ACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAA 291

Qy     87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
Db    292 AACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTG 351

Qy    107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
Db    352 TATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCAC 411

Qy    127 ProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIleLeuIleSerLeuAlaIle 146
Db    412 CCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTG 471

Qy    147 TrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
Db    472 TGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAACAGG 531

Qy    167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle 186
Db    532 ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGG 591

Qy    187 TyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCysPhePhe 206
Db    592 TACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGC 651

Qy    207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db    652 TATACCACGATT---ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG 708

Qy    227 LeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThr 246
Db    709 ---CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTA 765

Qy    247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
Db    766 CCCTTCCATATCTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCA---------ATC 816
```

```
Qy     267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
           |||:::   :::      |||:::      ||||||||||:::|||||||||||||
Db     817 AGTTGTTCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCT 876

Qy     286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
           |||||||:::      |||   :::   |||   ::::::   |||:::|||:::
Db     877 CTGAACACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCT 936

Qy     306 LeuMetAsnGlnLeuArg 311
           :::   :::   :::|||
Db     937 GTCTGCTCAACAGTGAGA 954

RESULT 13
ABQ78847
ID   ABQ78847 standard; cDNA; 1014 BP.
XX
AC   ABQ78847;
XX
DT   04-OCT-2002  (first entry)
XX
DE   Human G-protein coupled receptor PFI-019 cDNA.
XX
KW   Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective;
KW   anti-inflammatory; cytostatic; cardiovascular; antiallergic; hypotensive;
KW   antiarteriosclerotic; osteopathic; hypertension; asthma;
KW   artherosclerosis; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1014
FT                   /*tag= a
FT                   /product= "PFI-019"
XX
PN   EP1219638-A2.
XX
PD   03-JUL-2002.
XX
PF   04-DEC-2001; 2001EP-0310136.
XX
PR   18-DEC-2000; 2000GB-0030854.
PR   04-MAY-2001; 2001GB-0011031.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock MD;
XX
DR   WPI; 2002-521945/56.
DR   P-PSDB; ABB81902.
XX
PT   New G-protein coupled receptor (GPCR) polypeptide with homology to P2Y
PT   purinoreceptor, useful for treating e.g. inflammation or cancers in a
PT   patient, or for screening GPCR agonists or antagonists for treating
PT   these diseases -
XX
PS   Claim 1; Page 12; 19pp; English.
XX
CC   The invention relates to a novel G-protein coupled receptor (GPCR), and
CC   the polynucleotide encoding it. The protein of the invention has
CC   neuroprotective, anti-inflammatory, cytostatic, cardiovascular,
CC   antiallergic, hypotensive, antiarteriosclerotic, and osteopathic
CC   activity. The GPCR polypeptide is useful for manufacturing a medicament
CC   for treating a patient who needs to upregulate a receptor. Preferably,
CC   therapeutically useful areas are hypertension, asthma, and
CC   artherosclerosis. The sequence encodes the G-protein coupled receptor
CC   of the invention, PFI-019.
XX
SQ   Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Alignment Scores:
Pred. No.:              3.3e-37        Length:        1014
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```
Score:                  477.00         Matches:       110
Percent Similarity:     55.88%         Conservative:  61
Best Local Similarity:  35.95%         Mismatches:    123
Query Match:            27.30%         Indels:        12
DB:                     24             Gaps:          6

US-09-765-034-2 (1-334) x ABQ78847 (1-1014)

Qy       8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyrTyrLeuSer 27
           |||   |||   :::|||                          |||:::   :::|||||||
Db      67 AATTGCACTGATGAAAAC--------------ATCCCACTCAAGATGCACTACCTCCCT 111

Qy      28 IlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyrGly 47
           :::   |||||||||   |||:::|||||      ||||||   :::|||:::
Db     112 GTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACT 171

Qy      48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
           |||||||||   ::::::   |||   ||||||   |||   :::   |||||||:::
Db     172 TACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGC 231

Qy      68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsnGly--- 86
           :::|||||||   :::|||   :::||||||   ||||||      ||||||:::|||
Db     232 ACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAA 291

Qy      87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
           |||||||||:::||||||   :::|||         |||:::      |||   ||||||
Db     292 AACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTG 351

Qy     107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
           |||:::||||||||||||||||||||      ||||||   ||||||   :::|||   :::
Db     352 TATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCAC 411

Qy     127 ProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIleLeuIleSerLeuAlaIle 146
           |||                 :::   |||         |||::::::               :::
Db     412 CCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTG 471

Qy     147 TrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
           |||::::::      :::   ::::::|||:::      ||||||
Db     472 TGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAACAGG 531

Qy     167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle 186
           |||   :::   |||   |||      ||||||   :::   |||
Db     532 ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGG 591

Qy     187 TyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCysPhePhe 206
           |||:::::   ||||||         |||   :::||||||   ::::::
Db     592 TACAACCTAATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGC 651

Qy     207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
           |||   |||   :::                          |||      :::   |||
Db     652 TATACCACGATT---ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG 708

Qy     227 LeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThr 246
           :::|||      |||   |||:::   ::::::   |||   |||   |||
Db     709 ---CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTA 765

Qy     247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
           |||:::|||::::::|||   :::|||||||   |||||||||   |||
Db     766 CCCTTCCATATCTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCA---------ATC 816

Qy     267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
           |||:::   :::      |||:::      ||||||||||:::|||||||||||||
Db     817 AGTTGTTCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCT 876

Qy     286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
           |||||||:::      |||   :::   |||   ::::::   |||:::|||:::
Db     877 CTGAACACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCT 936

Qy     306 LeuMetAsnGlnLeuArg 311
           :::   :::   :::|||
Db     937 GTCTGCTCAACAGTGAGA 954

RESULT 14
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```
ABN85630
ID   ABN85630 standard; DNA; 1014 BP.
XX
AC   ABN85630;
XX
DT   18-SEP-2002  (first entry)
XX
DE   Human P2Y-like receptor variant encoding gene SEQ ID NO 3.
XX
KW   Human; Py2-like receptor; HIPHUM 0000037; immunity; inflammation;
KW   cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
KW   immunomodulator; anti-inflammatory; cytostatic; antiasthmatic;
KW   gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virucide;
KW   antibacterial; immunosuppressive; dermatological; nephrotropic;
KW   antiallergic; analgesic; receptor; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1014
FT                   /*tag= a
FT                   /product= "P2Y-like receptor variant"
XX
PN   GB2369364-A.
XX
PD   29-MAY-2002.
XX
PF   31-AUG-2001; 2001GB-0021215.
XX
PR   01-SEP-2000; 2000GB-0021524.
PR   06-SEP-2000; 2000GB-0021894.
PR   25-SEP-2000; 2000GB-0023444.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Foord SM,  Ignar DM;
XX
DR   WPI; 2002-511268/55.
DR   P-PSDB; ABB83819.
XX
PT   An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can be
PT   used for the identification of agonists and antagonists which may be
PT   used to treat an immune or inflammatory disease -
XX
PS   Claim 5; Page 28-29; 35pp; English.
XX
CC   The invention relates to an isolated P2Y-like receptor polypeptide
CC   (ABB83818-ABB83819) which is also referred to in the specification as
CC   HIPHUM 0000037. An effective amount of a substance (agonist or
CC   antagonist) which modulates P2Y receptor activity is useful to treat a
CC   subject having a disorder that is responsive to P2Y-like receptor
CC   modulation. The disorder is a disease of immunity or inflammation. The
CC   substance may also be used to manufacture a medicine for the treatment or
CC   prophylaxis of a disorder that is responsive to stimulation or modulation
CC   of P2Y-like receptor activity. Disorders which may be treated include
CC   colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
CC   gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
CC   colitis, rheumatoid arthritis, viral diseases, bacterial infections,
CC   autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
CC   rhinitis, inflammatory pain and general inflammation such as tendonitis,
CC   polymyositis or prostatitis. The invention provides alternative
CC   substances for the treatment of immunological and inflammatory diseases.
CC   The present sequence is that the P2Y-like receptor variant encoding gene
CC   of the invention.
XX
SQ   Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Alignment Scores:
Pred. No.:              3.3e-37        Length:          1014
Score:                  477.00         Matches:         110
Percent Similarity:     55.88%         Conservative:    61
Best Local Similarity:  35.95%         Mismatches:      123
Query Match:            27.30%         Indels:          12

DB:                     24             Gaps:            6

US-09-765-034-2 (1-334) x ABN85630 (1-1014)

Qy       8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyrTyrLeuSer 27
           |||   |||   :::|||                          |||:::   :::||||||
Db      67 AATTGCACTGATGAAAAC--------------ATCCCACTCAAGATGCACTACCTCCCT 111

Qy      28 IlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyrGly 47
           :::   |||||||||   |||:::|||||       ||||||   :::|||:::
Db     112 GTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACT 171

Qy      48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
           ||||||||   ::::::   |||   ||||||   |||   :::   ||||||:::
Db     172 TACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGC 231

Qy      68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsnGly--- 86
           :::|||||||   :::|||   :::|||||||   ||||||       ||||||:::|||
Db     232 ACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAA 291

Qy      87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
           |||||||||:::|||||   :::|||          |||:::      |||   ||||||
Db     292 AACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTG 351

Qy     107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
           |||:::|||||||||||||||||||       ||||||   ||||||   :::|||   :::
Db     352 TATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCAC 411

Qy     127 ProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIleLeuIleSerLeuAlaIle 146
           |||                  :::   |||          |||::::::           :::
Db     412 CCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTG 471

Qy     147 TrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
           |||::::::      :::   ::::::|||:::      ||||||
Db     472 TGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAACAGG 531

Qy     167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle 186
             |||   :::   |||   |||       ||||||   :::   |||
Db     532 ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGG 591

Qy     187 TyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCysPhePhe 206
           |||::::::   ||||||         |||   :::||||||   ::::::
Db     592 TACAACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGC 651

Qy     207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
           |||       |||   :::                        |||       :::   |||
Db     652 TATACCACGATT---ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG 708

Qy     227 LeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThr 246
             :::|||          |||   |||:::   ::::::   |||   |||   |||
Db     709 ---CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTA 765

Qy     247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
           |||:::|||:::::::|||   :::|||||||   |||||||||   |||
Db     766 CCCTTCCATATCTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCA---------ATC 816

Qy     267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
           |||:::   :::       |||:::       ||||||||||:::||||||||||||
Db     817 AGTTGTTCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCT 876

Qy     286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
           ||||||:::       |||   :::   |||   ::::::   |||:::|||:::
Db     877 CTGAACACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCT 936

Qy     306 LeuMetAsnGlnLeuArg 311
           :::   :::   :::|||
Db     937 GTCTGCTCAACAGTGAGA 954

RESULT 15
AAD34278
ID   AAD34278 standard; cDNA; 1014 BP.
XX
AC   AAD34278;
```

```
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human AXOR89 (G-protein coupled receptor) cDNA.
XX
KW   Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;
KW   infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity;
KW   anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;
KW   stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;
KW   myocardial infarction; allergy; benign prostatic hypertrophy; migraine;
KW   vomitting; psychotic; neurological disorder; anxiety; manic depression;
KW   delirium; Huntington's Disease; Gilles dela Tourette's syndrome;
KW   dementia; dyskinesia; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1014
FT                   /*tag= a
FT                   /product= "Human AXOR89 protein"
XX
PN   GB2365012-A.
XX
PD   13-FEB-2002.
XX
PF   10-MAY-2001; 2001GB-0011437.
XX
PR   11-MAY-2000; 2000US-0569137.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Elshourbagy N,  Shabon U;
XX
DR   WPI; 2002-332558/37.
DR   P-PSDB; AAE21803.
XX
PT   Novel AXOR89 polypeptide and polynucleotide encoding it, useful for
PT   identifying agonists and antagonists in the treatment of diseases
PT   associated with an AXOR89 imbalance, such as cancers, diabetes or
PT   asthma -
XX
PS   Claim 2; Page 30; 37pp; English.
XX
CC   The invention relates to an isolated AXOR89 polypeptide (G-protein
CC   coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
CC   and polynucleotide encoding the polypeptide, is useful for identifying
CC   agonists and antagonists (or inhibitors) that are potentially useful in
CC   treating conditions associated with an AXOR89 imbalance, such as
CC   bacterial, fungal or protozoan infections, cancers, pain, asthma,
CC   Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart
CC   failure, hypotension, hypertension, urinary retention, osteoporosis,
CC   angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
CC   prostatic hypertrophy, migraine, vomitting, psychotic and neurological
CC   disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
CC   dyskinesias, such as Huntington's Disease or Gilles dela Tourette's
CC   syndrome. The polynucleotide sequence may also be used for chromosome
CC   localisation or tissue expression studies. The AXOR89 is used as a
CC   vaccine or to produce fusion proteins. The present sequence is human
CC   AXOR89 cDNA.
XX
SQ   Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Alignment Scores:
Pred. No.:                3.3e-37        Length:          1014
Score:                    477.00         Matches:         110
Percent Similarity:       55.88%         Conservative:    61
Best Local Similarity:    35.95%         Mismatches:      123
Query Match:              27.30%         Indels:          12
DB:                       24             Gaps:            6

US-09-765-034-2 (1-334) x AAD34278 (1-1014)

Qy       8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyrTyrLeuSer 27
Db      67 AATTGCACTGATGAAAAC--------------ATCCCACTCAAGATGCACTACCTCCCT 111

Qy      28 IlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyrGly 47
Db     112 GTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACT 171

Qy      48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
Db     172 TACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGC 231

Qy      68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsnGly--- 86
Db     232 ACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAA 291

Qy      87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
Db     292 AACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTG 351

Qy     107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
Db     352 TATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCAC 411

Qy     127 ProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIleLeuIleSerLeuAlaIle 146
Db     412 CCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTG 471

Qy     147 TrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
Db     472 TGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAACAGG 531

Qy     167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle 186
Db     532 ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGG 591

Qy     187 TyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCysPhePhe 206
Db     592 TACAACCTAATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGC 651

Qy     207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db     652 TATACCACGATT---ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG 708

Qy     227 LeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThr 246
Db     709 ---CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTA 765

Qy     247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
Db     766 CCCTTCCATATCTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCA---------ATC 816

Qy     267 GlnCysThr---GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
Db     817 AGTTGTTCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCT 876

Qy     286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
Db     877 CTGAACACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCT 936

Qy     306 LeuMetAsnGlnLeuArg 311
Db     937 GTCTGCTCAACAGTGAGA 954


Search completed: December  9, 2002, 12:22:56
Job time : 290 secs
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